SEQUENCE LISTING

<110>   US ONLY:
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         OTHER COUNTRIES:
         Agriculture Victoria Services Pty Ltd AND Pig Research and Development
         Corporation AND Pfizer Products Inc.

<120> Novel therapeutic compositions for treating infection by *Lawsonia spp.*

<130>

<150> AU PR1381
<151> 2000-11-10
<150> US 60/249596
<151> 2000-11-17

<160> 68

<170> PatentIn Ver. 2.0

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cag gaa gct cgt tct gaa ggg agt gtc cct aaa tca gaa gag gtt act   96
Gln Glu Ala Arg Ser Glu Gly Ser Val Pro Lys Ser Glu Glu Val Thr
            20   25   30

aaa gca ttg act act gca gca ggg atg ctg ggg ctt gct att tat tca   144
Lys Ala Leu Thr Thr Ala Ala Gly Met Leu Gly Leu Ala Ile Tyr Ser
            35   40   45

ggc gta atg gga cgt cat ttt gaa aca att ttc tac tat att ttt aca   192
Gly Val Met Gly Arg His Phe Glu Thr Ile Phe Tyr Tyr Ile Phe Thr

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                    50                      55                      60

        gaa tca ttt cgg ttt gag gtt aca gca cag tca gta tat gct tta ttt    240
        Glu Ser Phe Arg Phe Glu Val Thr Ala Gln Ser Val Tyr Ala Leu Phe
  5     65                  70                  75                  80

        att tat gtt gct caa gag ata gct att tta ttg atg cca ata tta ctt    288
        Ile Tyr Val Ala Gln Glu Ile Ala Ile Leu Leu Met Pro Ile Leu Leu
                            85                  90                  95
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        ttt att gct gtt acg gca tgg att tca tta cgt gta caa gtt ggt gca    336
        Phe Ile Ala Val Thr Ala Trp Ile Ser Leu Arg Val Gln Val Gly Ala
                        100                 105                 110

 15     tta tgg act aca aag gtt ttt aaa ttt aaa tgg agt aaa ttt aat ata    384
        Leu Trp Thr Thr Lys Val Phe Lys Phe Lys Trp Ser Lys Phe Asn Ile
                    115                 120                 125

        ata aaa ggg ttg aaa gga atg ttt gct tct caa caa aca ctt gtt cga    432
 20     Ile Lys Gly Leu Lys Gly Met Phe Ala Ser Gln Gln Thr Leu Val Arg
                130                 135                 140

        ctt tta cgt agt tta gtt caa gta att gtt ata ggt att gtt cca tat    480
        Leu Leu Arg Ser Leu Val Gln Val Ile Val Ile Gly Ile Val Pro Tyr
 25     145                 150                 155                 160

        atg att ata aaa gga gag ttt tca aac ttt tta cca tta tat tat gca    528
        Met Ile Ile Lys Gly Glu Phe Ser Asn Phe Leu Pro Leu Tyr Tyr Ala
                            165                 170                 175
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        agt cct tca ggt gtg gca gat tat atg ctt aat aca gga ata gta ctt    576
        Ser Pro Ser Gly Val Ala Asp Tyr Met Leu Asn Thr Gly Ile Val Leu
                        180                 185                 190

 35     gtt tta tat acg cta att cct atg aca att att gca gtc gca gat c       622
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                 35                  40                  45

    Gly Val Met Gly Arg His Phe Glu Thr Ile Phe Tyr Tyr Ile Phe Thr
            50                  55                  60

    Glu Ser Phe Arg Phe Glu Val Thr Ala Gln Ser Val Tyr Ala Leu Phe
    65                  70                  75                  80

    Ile Tyr Val Ala Gln Glu Ile Ala Ile Leu Leu Met Pro Ile Leu Leu
                     85                  90                  95

    Phe Ile Ala Val Thr Ala Trp Ile Ser Leu Arg Val Gln Val Gly Ala
                100                 105                 110

    Leu Trp Thr Thr Lys Val Phe Lys Phe Lys Trp Ser Lys Phe Asn Ile
            115                 120                 125

    Ile Lys Gly Leu Lys Gly Met Phe Ala Ser Gln Gln Thr Leu Val Arg
        130                 135                 140

    Leu Leu Arg Ser Leu Val Gln Val Ile Val Ile Gly Ile Val Pro Tyr
    145                 150                 155                 160

    Met Ile Ile Lys Gly Glu Phe Ser Asn Phe Leu Pro Leu Tyr Tyr Ala
                165                 170                 175

    Ser Pro Ser Gly Val Ala Asp Tyr Met Leu Asn Thr Gly Ile Val Leu
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    Val Leu Tyr Thr Leu Ile Pro Met Thr Ile Ile Ala Val Ala Asp
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  1               5                  10                  15

aca ttt tta cgt att agt gtt gtc tta ttt atg ctt cct ttt ttt tct    96
Thr Phe Leu Arg Ile Ser Val Val Leu Phe Met Leu Pro Phe Phe Ser
             20                  25                  30

att gat ggt ttt cct aat atg tta aaa gca tca ata gct ctt att cta   144
Ile Asp Gly Phe Pro Asn Met Leu Lys Ala Ser Ile Ala Leu Ile Leu
         35                  40                  45

act ata gtt ctt tgg ggg cgt ctt tct ctt tca gga aca caa atg cca   192
Thr Ile Val Leu Trp Gly Arg Leu Ser Leu Ser Gly Thr Gln Met Pro
     50                  55                  60

gcg cat cct ttc gat cta gta ttg tta atc ata agc gag gtt ttt ctt   240
Ala His Pro Phe Asp Leu Val Leu Leu Ile Ile Ser Glu Val Phe Leu
 65                  70                  75                  80

ggt att gta ttg ggg ctt gcg gta aac ttt ttc ttt gca gga att caa   288
Gly Ile Val Leu Gly Leu Ala Val Asn Phe Phe Phe Ala Gly Ile Gln
                 85                  90                  95

gct ggg gga gaa att ctt gct aca caa atg ggg ttt aca atg att acg   336
Ala Gly Gly Glu Ile Leu Ala Thr Gln Met Gly Phe Thr Met Ile Thr
                100                 105                 110

ctt gca gac cca tta act ggt aac acc aca ggt ttt att gca cat ttt   384
Leu Ala Asp Pro Leu Thr Gly Asn Thr Thr Gly Phe Ile Ala His Phe
            115                 120                 125

ctt tat atg gtt gct aca tta gtt ttt ctt gct ctt aat ggc cat ttg   432
Leu Tyr Met Val Ala Thr Leu Val Phe Leu Ala Leu Asn Gly His Leu
            130                 135                 140

ttt ctt ata aaa gct ttt aca tat act ttt aaa atg gtt cca gca gga   480
Phe Leu Ile Lys Ala Phe Thr Tyr Thr Phe Lys Met Val Pro Ala Gly
145                 150                 155                 160

gga ctt gtt gta aga gaa att tta ttg agt gaa ctt ctt aat atg gca   528
Gly Leu Val Val Arg Glu Ile Leu Leu Ser Glu Leu Leu Asn Met Ala
                165                 170                 175
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ggg atg att ttt gtt ttt gcc tta cat gtt gcg gca cca gtt atg tca    576
Gly Met Ile Phe Val Phe Ala Leu His Val Ala Ala Pro Val Met Ser
            180                 185                 190

gct ctt ttt tta gta gag atc tct tta gga ctt atg gca aga gct gct    624
Ala Leu Phe Leu Val Glu Ile Ser Leu Gly Leu Met Ala Arg Ala Ala
            195                 200                 205

cct cag att cat att atg gaa gtt gga ttt cct gta aaa att ggt gta    672
Pro Gln Ile His Ile Met Glu Val Gly Phe Pro Val Lys Ile Gly Val
            210                 215                 220

gga ttt ttt ttc att gga cta tta ttt act atc tta tca aaa gaa acc    720
Gly Phe Phe Phe Ile Gly Leu Leu Phe Thr Ile Leu Ser Lys Glu Thr
225                 230                 235                 240

tat cga ttt att gca ggc cta gag gga cta ttt ttt aac tta ctt act    768
Tyr Arg Phe Ile Ala Gly Leu Glu Gly Leu Phe Phe Asn Leu Leu Thr
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gta atg ggt agt gga aaa tag                                        789
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Thr Phe Leu Arg Ile Ser Val Val Leu Phe Met Leu Pro Phe Phe Ser
            20                  25                  30

Ile Asp Gly Phe Pro Asn Met Leu Lys Ala Ser Ile Ala Leu Ile Leu
            35                  40                  45

Thr Ile Val Leu Trp Gly Arg Leu Ser Leu Ser Gly Thr Gln Met Pro
            50                  55                  60

Ala His Pro Phe Asp Leu Val Leu Leu Ile Ile Ser Glu Val Phe Leu
  65                  70                  75                  80
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Gly Ile Val Leu Gly Leu Ala Val Asn Phe Phe Phe Ala Gly Ile Gln
                85   90   95

5   Ala Gly Gly Glu Ile Leu Ala Thr Gln Met Gly Phe Thr Met Ile Thr
                   100   105   110

Leu Ala Asp Pro Leu Thr Gly Asn Thr Thr Gly Phe Ile Ala His Phe
              115   120   125

10

Leu Tyr Met Val Ala Thr Leu Val Phe Leu Ala Leu Asn Gly His Leu
              130   135   140

Phe Leu Ile Lys Ala Phe Thr Tyr Thr Phe Lys Met Val Pro Ala Gly
15 145   150   155   160

Gly Leu Val Val Arg Glu Ile Leu Leu Ser Glu Leu Leu Asn Met Ala
                   165   170   175

20 Gly Met Ile Phe Val Phe Ala Leu His Val Ala Ala Pro Val Met Ser
                   180   185   190

Ala Leu Phe Leu Val Glu Ile Ser Leu Gly Leu Met Ala Arg Ala Ala
              195   200   205

25

Pro Gln Ile His Ile Met Glu Val Gly Phe Pro Val Lys Ile Gly Val
       210   215   220

Gly Phe Phe Phe Ile Gly Leu Leu Phe Thr Ile Leu Ser Lys Glu Thr
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Tyr Arg Phe Ile Ala Gly Leu Glu Gly Leu Phe Phe Asn Leu Leu Thr
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 1               5                   10                  15

ca ttg aaa gga att ttt gaa gat gag ggc cat gaa gtt tta gaa aga     96
Ser Leu Lys Gly Ile Phe Glu Asp Glu Gly His Glu Val Leu Glu Arg
                 20                  25                  30

gct tca gca gaa gaa gga ctt aag tgt gtt gat gta gag tct cca gat   144
Ala Ser Ala Glu Glu Gly Leu Lys Cys Val Asp Val Glu Ser Pro Asp
            35                  40                  45

ctt gtt ttt ctt gat att tgg ctt cct ggg atg gat ggt ctt atg gct   192
Leu Val Phe Leu Asp Ile Trp Leu Pro Gly Met Asp Gly Leu Met Ala
        50                  55                  60

tta gac cat att cag gct ctt cat cag gaa tta cct gtt att atg att   240
Leu Asp His Ile Gln Ala Leu His Gln Glu Leu Pro Val Ile Met Ile
  65                  70                  75                  80

tca ggt cat gcc aca att gaa act gct gta aca gct atc cgt caa ggt   288
Ser Gly His Ala Thr Ile Glu Thr Ala Val Thr Ala Ile Arg Gln Gly
                85                  90                  95

gct tat gat ttt att gaa aag cct ctt tct ttg gaa aaa gtc ctt att   336
Ala Tyr Asp Phe Ile Glu Lys Pro Leu Ser Leu Glu Lys Val Leu Ile
               100                 105                 110

aca gct aat aga gct ata gaa aca gta aga tta aga agg gaa aac aaa   384
Thr Ala Asn Arg Ala Ile Glu Thr Val Arg Leu Arg Arg Glu Asn Lys
            115                 120                 125

tta cta cgt act gta tta cct gag gag agt gag ttt ata gga cag tct   432
Leu Leu Arg Thr Val Leu Pro Glu Glu Ser Glu Phe Ile Gly Gln Ser
        130                 135                 140

cct gtt atc tta aaa ttt aaa agt tta tta tca cag gtc gct cca aca   480
Pro Val Ile Leu Lys Phe Lys Ser Leu Leu Ser Gln Val Ala Pro Thr
145                 150                 155                 160

gat gct tgg gta cta ctt aca gga gag aat ggt aca ggt aaa gag tta   528
Asp Ala Trp Val Leu Leu Thr Gly Glu Asn Gly Thr Gly Lys Glu Leu
               165                 170                 175
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      gct gca caa gca ttg cac aaa gga agc tca cga tat caa aaa cca ttt    576
      Ala Ala Gln Ala Leu His Lys Gly Ser Ser Arg Tyr Gln Lys Pro Phe
                      180                 185                 190

  5   ata gct gtt aat tgt gct gct atc cct gaa gaa ttg att gaa agc gaa    624
      Ile Ala Val Asn Cys Ala Ala Ile Pro Glu Glu Leu Ile Glu Ser Glu
                      195                 200                 205

      cta ttt ggt cat gaa aaa ggg gcc ttt act ggt gcc gat gct tct cgt    672
 10   Leu Phe Gly His Glu Lys Gly Ala Phe Thr Gly Ala Asp Ala Ser Arg
                      210                 215                 220

      gca ggt cgt ttt gag ttg gca cat aaa gga aca tta ttt ctt gat gaa    720
      Ala Gly Arg Phe Glu Leu Ala His Lys Gly Thr Leu Phe Leu Asp Glu
 15   225                 230                 235                 240

      ata gga gat atg agt tta aaa aca caa gca aaa att ttg cgt att ttg    768
      Ile Gly Asp Met Ser Leu Lys Thr Gln Ala Lys Ile Leu Arg Ile Leu
                      245                 250                 255
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      caa gaa caa tgt ttt gaa aaa att ggt agt gtt aga act att aaa gtt    816
      Gln Glu Gln Cys Phe Glu Lys Ile Gly Ser Val Arg Thr Ile Lys Val
                      260                 265                 270

 25   gat gta aga gtt att gca gca aca aat aag aat ctt gaa gac gct att    864
      Asp Val Arg Val Ile Ala Ala Thr Asn Lys Asn Leu Glu Asp Ala Ile
                      275                 280                 285

      agc gat gga aca ttt cgt caa gat ttg tat tat cgc tta cga gtt gtt    912
 30   Ser Asp Gly Thr Phe Arg Gln Asp Leu Tyr Tyr Arg Leu Arg Val Val
                      290                 295                 300

      cca ttg cat ctt ccc cct ctt cgt gaa cgt gat tct gat att gag cta    960
      Pro Leu His Leu Pro Pro Leu Arg Glu Arg Asp Ser Asp Ile Glu Leu
 35   305                 310                 315                 320

      tta tta aat agg ttt gtg att cag ttg agt aaa cgt tat aga cgt gag   1008
      Leu Leu Asn Arg Phe Val Ile Gln Leu Ser Lys Arg Tyr Arg Arg Glu
                      325                 330                 335
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      ccg cct att ttt tta gat gag gtc ttc cct gta ttg aaa caa tat tgt   1056
      Pro Pro Ile Phe Leu Asp Glu Val Phe Pro Val Leu Lys Gln Tyr Cys
                      340                 345                 350

 45   tgg cca ggg aat gta aga gaa tta ctt aat ttt gta gaa cga atg gtt   1104
      Trp Pro Gly Asn Val Arg Glu Leu Leu Asn Phe Val Glu Arg Met Val
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                    355                 360                 365

      att ctt tat tca ggg aag aaa gta tgt ttg aca gat cct aag gta aaa    1152
      Ile Leu Tyr Ser Gly Lys Lys Val Cys Leu Thr Asp Pro Lys Val Lys
  5       370                 375                 380

      agc aat tta aaa tat tta ccc aag aaa ttt tct tcc cat tat aac ttt    1200
      Ser Asn Leu Lys Tyr Leu Pro Lys Lys Phe Ser Ser His Tyr Asn Phe
          385                 390                 395                 400
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      ctt ccc gat ata gat ttt aac cag gct aaa ata gct ttt gaa cca aaa    1248
      Leu Pro Asp Ile Asp Phe Asn Gln Ala Lys Ile Ala Phe Glu Pro Lys
                          405                 410                 415

 15   ttt tta act gaa aaa tta cat gct tat caa gga aat att acc cga tta    1296
      Phe Leu Thr Glu Lys Leu His Ala Tyr Gln Gly Asn Ile Thr Arg Leu
                      420                 425                 430

      gca gaa gct att gga ctt gaa aga agt tat tta tat aga aag cta aaa    1344
 20   Ala Glu Ala Ile Gly Leu Glu Arg Ser Tyr Leu Tyr Arg Lys Leu Lys
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      agc tat ggt att tat ctg tct gag tga                              1371
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 25       450                 455



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                  20                  25                  30

 40   Ala Ser Ala Glu Glu Gly Leu Lys Cys Val Asp Val Glu Ser Pro Asp
              35                  40                  45

      Leu Val Phe Leu Asp Ile Trp Leu Pro Gly Met Asp Gly Leu Met Ala
          50                  55                  60
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      Leu Asp His Ile Gln Ala Leu His Gln Glu Leu Pro Val Ile Met Ile
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          65                    70                    75                    80


         Ser Gly His Ala Thr Ile Glu Thr Ala Val Thr Ala Ile Arg Gln Gly
                         85                    90                    95
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         Ala Tyr Asp Phe Ile Glu Lys Pro Leu Ser Leu Glu Lys Val Leu Ile
                        100                   105                   110

         Thr Ala Asn Arg Ala Ile Glu Thr Val Arg Leu Arg Arg Glu Asn Lys
 10                 115                   120                   125

         Leu Leu Arg Thr Val Leu Pro Glu Glu Ser Glu Phe Ile Gly Gln Ser
                    130                   135                   140

 15      Pro Val Ile Leu Lys Phe Lys Ser Leu Leu Ser Gln Val Ala Pro Thr
         145                   150                   155                   160

         Asp Ala Trp Val Leu Leu Thr Gly Glu Asn Gly Thr Gly Lys Glu Leu
                        165                   170                   175
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         Ala Ala Gln Ala Leu His Lys Gly Ser Ser Arg Tyr Gln Lys Pro Phe
                        180                   185                   190

         Ile Ala Val Asn Cys Ala Ala Ile Pro Glu Glu Leu Ile Glu Ser Glu
 25                 195                   200                   205

         Leu Phe Gly His Glu Lys Gly Ala Phe Thr Gly Ala Asp Ala Ser Arg
                    210                   215                   220

 30      Ala Gly Arg Phe Glu Leu Ala His Lys Gly Thr Leu Phe Leu Asp Glu
         225                   230                   235                   240

         Ile Gly Asp Met Ser Leu Lys Thr Gln Ala Lys Ile Leu Arg Ile Leu
                        245                   250                   255
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         Gln Glu Gln Cys Phe Glu Lys Ile Gly Ser Val Arg Thr Ile Lys Val
                        260                   265                   270

         Asp Val Arg Val Ile Ala Ala Thr Asn Lys Asn Leu Glu Asp Ala Ile
 40                 275                   280                   285

         Ser Asp Gly Thr Phe Arg Gln Asp Leu Tyr Tyr Arg Leu Arg Val Val
                    290                   295                   300

 45      Pro Leu His Leu Pro Pro Leu Arg Glu Arg Asp Ser Asp Ile Glu Leu
         305                   310                   315                   320
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        Leu Leu Asn Arg Phe Val Ile Gln Leu Ser Lys Arg Tyr Arg Arg Glu
                    325             330             335
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                    340             345             350
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        Trp Pro Gly Asn Val Arg Glu Leu Leu Asn Phe Val Glu Arg Met Val
                    355             360             365
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        Ile Leu Tyr Ser Gly Lys Lys Val Cys Leu Thr Asp Pro Lys Val Lys
                   370             375             380
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        Ser Asn Leu Lys Tyr Leu Pro Lys Lys Phe Ser Ser His Tyr Asn Phe
  15    385                 390             395                 400
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        Leu Pro Asp Ile Asp Phe Asn Gln Ala Lys Ile Ala Phe Glu Pro Lys
                        405             410                 415
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  20    Phe Leu Thr Glu Lys Leu His Ala Tyr Gln Gly Asn Ile Thr Arg Leu
                    420                 425             430
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        Ala Glu Ala Ile Gly Leu Glu Arg Ser Tyr Leu Tyr Arg Lys Leu Lys
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  25
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        Ser Tyr Gly Ile Tyr Leu Ser Glu
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<213> Lawsonia intracellularis

<220>
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<222> (1)..(411)

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 1               5                   10                  15
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aat ctt caa gtc aat ttt tct aac cca tac cat caa aca gat att gaa     96
Asn Leu Gln Val Asn Phe Ser Asn Pro Tyr His Gln Thr Asp Ile Glu
                20                  25                  30
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      gtc ctg gct aat gca aaa aaa gtt aaa ggg atg aag ttt cca caa gac   144
      Val Leu Ala Asn Ala Lys Lys Val Lys Gly Met Lys Phe Pro Gln Asp
              35                  40                  45

 5    ttt aat aaa cct gaa gtt ata gtt gct ata cgt aat ggt agt aca gtt   192
      Phe Asn Lys Pro Glu Val Ile Val Ala Ile Arg Asn Gly Ser Thr Val
              50                  55                  60

      att act cct gca aag caa ctt ctt cct aaa gca tct ttt aga ctc ttt   240
 10   Ile Thr Pro Ala Lys Gln Leu Leu Pro Lys Ala Ser Phe Arg Leu Phe
          65                  70                  75                  80

      gat gat gaa gtt gca tct ata aaa gat gta gaa tct gga caa tca cat   288
      Asp Asp Glu Val Ala Ser Ile Lys Asp Val Glu Ser Gly Gln Ser His
 15                       85                  90                  95

      ata tta tta gct tca gca cca tta cca gcg att caa gct ata aac tca   336
      Ile Leu Leu Ala Ser Ala Pro Leu Pro Ala Ile Gln Ala Ile Asn Ser
                      100                 105                 110
 20
      aat ggc aac ctt att cgt tta gat aca ctc ccc att act cat caa tct   384
      Asn Gly Asn Leu Ile Arg Leu Asp Thr Leu Pro Ile Thr His Gln Ser
                  115                 120                 125

 25   gta gga ttt gca ata aag aag gga gat c                            412
      Val Gly Phe Ala Ile Lys Lys Gly Asp
              130                 135
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      Asn Leu Gln Val Asn Phe Ser Asn Pro Tyr His Gln Thr Asp Ile Glu
 40                   20                  25                  30

      Val Leu Ala Asn Ala Lys Lys Val Lys Gly Met Lys Phe Pro Gln Asp
              35                  40                  45

 45   Phe Asn Lys Pro Glu Val Ile Val Ala Ile Arg Asn Gly Ser Thr Val
              50                  55                  60
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    Ile Thr Pro Ala Lys Gln Leu Leu Pro Lys Ala Ser Phe Arg Leu Phe
    65                  70                  75                  80

5   Asp Asp Glu Val Ala Ser Ile Lys Asp Val Glu Ser Gly Gln Ser His
                        85                  90                  95

    Ile Leu Leu Ala Ser Ala Pro Leu Pro Ala Ile Gln Ala Ile Asn Ser
                    100                 105                 110
10
    Asn Gly Asn Leu Ile Arg Leu Asp Thr Leu Pro Ile Thr His Gln Ser
                115                 120                 125


    Val Gly Phe Ala Ile Lys Lys Gly Asp
15          130                 135



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20  <212> DNA
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30   1               5                  10                  15


    ggc tac ctt atg gct aaa ggg aat ctt gct tta ctc ttt caa cct gca     96
    Gly Tyr Leu Met Ala Lys Gly Asn Leu Ala Leu Leu Phe Gln Pro Ala
                    20                  25                  30
35
    gaa ctt gtt atc att att ggg gca gca tta ggt gct ttt ttt gct tca    144
    Glu Leu Val Ile Ile Ile Gly Ala Ala Leu Gly Ala Phe Phe Ala Ser
                35                  40                  45


40  cag acg aaa tat tca ttt act ctg gtc att aaa aat tta tca cac att    192
    Gln Thr Lys Tyr Ser Phe Thr Leu Val Ile Lys Asn Leu Ser His Ile
            50                  55                  60


    ttt ggc gat cca aac agt aca aaa ata aaa tac ctt gaa aca ctt gcc    240
45  Phe Gly Asp Pro Asn Ser Thr Lys Ile Lys Tyr Leu Glu Thr Leu Ala
        65                  70                  75                  80
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      ctt ctc tat gga ctt ttc tta aaa atg aat aga gaa ggt gtc att agt    288
      Leu Leu Tyr Gly Leu Phe Leu Lys Met Asn Arg Glu Gly Val Ile Ser
                      85                  90                  95
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      ata gaa agt gat ata gaa aaa cct gaa tca agt cct atc ttt agt aaa    336
      Ile Glu Ser Asp Ile Glu Lys Pro Glu Ser Ser Pro Ile Phe Ser Lys
                     100                 105                 110

10    tac cct aca att gta aaa gat act aaa gtt gtt gcc ttt att gca gat    384
      Tyr Pro Thr Ile Val Lys Asp Thr Lys Val Val Ala Phe Ile Ala Asp
                     115                 120                 125

      aca tta cga gtt tat ctg aca aca ggt gca cca gaa gat ata gat aac    432
15    Thr Leu Arg Val Tyr Leu Thr Thr Gly Ala Pro Glu Asp Ile Asp Asn
                 130                 135                 140

      ctc atg gaa tct gac atg aaa att aca cac gaa gaa gaa tta tta cct    480
      Leu Met Glu Ser Asp Met Lys Ile Thr His Glu Glu Glu Leu Leu Pro
20    145                 150                 155                 160

      gca cat tcc atc agc cat atg gca gag tcg cta cca gga atg ggt att    528
      Ala His Ser Ile Ser His Met Ala Glu Ser Leu Pro Gly Met Gly Ile
                     165                 170                 175
25
      gtt gct gca gta tta ggt gtt gtt att acc atg gga aaa att aat gag    576
      Val Ala Ala Val Leu Gly Val Val Ile Thr Met Gly Lys Ile Asn Glu
                     180                 185                 190

30    cct cca gaa gtc ctt ggg cat tat att gga gca gct ttg gtt ggt aca    624
      Pro Pro Glu Val Leu Gly His Tyr Ile Gly Ala Ala Leu Val Gly Thr
                     195                 200                 205

      ttt ata ggt att ctt ttc tgt tat ggt ttt ttt gga cct atg ggt tca    672
35    Phe Ile Gly Ile Leu Phe Cys Tyr Gly Phe Phe Gly Pro Met Gly Ser
                 210                 215                 220

      aag ctt gaa acc tct gca gaa gaa gca cat ttt tat tat aat tcc att    720
      Lys Leu Glu Thr Ser Ala Glu Glu Ala His Phe Tyr Tyr Asn Ser Ile
40    225                 230                 235                 240

      aaa gaa gct gtt gca gct gct atc cga ggt tct aca cca atg ata gca    768
      Lys Glu Ala Val Ala Ala Ala Ile Arg Gly Ser Thr Pro Met Ile Ala
                     245                 250                 255
45
      gta gaa tat gga aga cgt gcc ata cct aat aca ttt cgt cca tca ttt    816
```

```
        Val Glu Tyr Gly Arg Arg Ala Ile Pro Asn Thr Phe Arg Pro Ser Phe
                    260             265             270

        tcg gaa atg gaa gaa cgt cta aaa aca gga taa                      849
    5   Ser Glu Met Glu Glu Arg Leu Lys Thr Gly
                    275             280


        <210> 10
   10   <211> 282
        <212> PRT
        <213> Lawsonia intracellularis


        <400> 10
   15   Met Tyr Ile Ile Ile Gly Tyr Phe Ile Val Ile Ala Ser Ile Ile Gly
         1               5              10                  15

        Gly Tyr Leu Met Ala Lys Gly Asn Leu Ala Leu Leu Phe Gln Pro Ala
                    20              25                  30
   20
        Glu Leu Val Ile Ile Ile Gly Ala Ala Leu Gly Ala Phe Phe Ala Ser
                35              40                  45

        Gln Thr Lys Tyr Ser Phe Thr Leu Val Ile Lys Asn Leu Ser His Ile
   25       50              55                  60

        Phe Gly Asp Pro Asn Ser Thr Lys Ile Lys Tyr Leu Glu Thr Leu Ala
         65              70              75                  80

   30   Leu Leu Tyr Gly Leu Phe Leu Lys Met Asn Arg Glu Gly Val Ile Ser
                        85              90                  95

        Ile Glu Ser Asp Ile Glu Lys Pro Glu Ser Ser Pro Ile Phe Ser Lys
                    100             105                 110
   35
        Tyr Pro Thr Ile Val Lys Asp Thr Lys Val Val Ala Phe Ile Ala Asp
                    115             120                 125

        Thr Leu Arg Val Tyr Leu Thr Thr Gly Ala Pro Glu Asp Ile Asp Asn
   40       130             135                 140

        Leu Met Glu Ser Asp Met Lys Ile Thr His Glu Glu Glu Leu Leu Pro
        145             150                 155                 160

   45   Ala His Ser Ile Ser His Met Ala Glu Ser Leu Pro Gly Met Gly Ile
                        165                 170                 175
```

```
       Val Ala Ala Val Leu Gly Val Val Ile Thr Met Gly Lys Ile Asn Glu
                   180                 185                 190

 5     Pro Pro Glu Val Leu Gly His Tyr Ile Gly Ala Ala Leu Val Gly Thr
                   195                 200                 205

       Phe Ile Gly Ile Leu Phe Cys Tyr Gly Phe Phe Gly Pro Met Gly Ser
                   210                 215                 220

10
       Lys Leu Glu Thr Ser Ala Glu Glu Ala His Phe Tyr Tyr Asn Ser Ile
       225                 230                 235                 240

       Lys Glu Ala Val Ala Ala Ala Ile Arg Gly Ser Thr Pro Met Ile Ala
15                         245                 250                 255

       Val Glu Tyr Gly Arg Arg Ala Ile Pro Asn Thr Phe Arg Pro Ser Phe
                   260                 265                 270

20     Ser Glu Met Glu Glu Arg Leu Lys Thr Gly
                   275                 280


       <210> 11
25     <211> 717
       <212> DNA
       <213> Lawsonia intracellularis

       <220>
30     <221> CDS
       <222> (1)..(714)


       <400> 11
       atg tct ggc tca tgg aaa gtg gct tat gca gac ttt gtt aca gct atg   48
35     Met Ser Gly Ser Trp Lys Val Ala Tyr Ala Asp Phe Val Thr Ala Met
         1               5                  10                  15

       atg gct ttc ttt cta ctg atg tgg att ctt gca atg aca ccc cct gag   96
       Met Ala Phe Phe Leu Leu Met Trp Ile Leu Ala Met Thr Pro Pro Glu
40                       20                  25                  30

       gtt aaa gaa ggt ctt gct gca tat ttt tct tca tct gat gct aca ttt  144
       Val Lys Glu Gly Leu Ala Ala Tyr Phe Ser Ser Ser Asp Ala Thr Phe
                   35                  40                  45

45
       aaa aca cct gat agt tcg cca atc tct aac aat cct ctt atc aac caa  192
```

```
        Lys Thr Pro Asp Ser Ser Pro Ile Ser Asn Asn Pro Leu Ile Asn Gln
             50                  55                  60

        ata gat aaa ctt gat act cga caa tta aaa att aat gaa aca gaa caa   240
    5   Ile Asp Lys Leu Asp Thr Arg Gln Leu Lys Ile Asn Glu Thr Glu Gln
        ·65                  70                  75                  80

        tct cat tat gct ctt gct aat aaa tta aaa aaa atg tta atg gct gat   288
        Ser His Tyr Ala Leu Ala Asn Lys Leu Lys Lys Met Leu Met Ala Asp
   10                       85                  90                  95

        gct atc cca cag tca gca aca gga ata agt gct gac gat gtt ggt gta   336
        Ala Ile Pro Gln Ser Ala Thr Gly Ile Ser Ala Asp Asp Val Gly Val
                        100                 105                 110
   15
        tta tta cgt gta aat tct aat tcc acg ttt ttt cct ggt aca gca act   384
        Leu Leu Arg Val Asn Ser Asn Ser Thr Phe Phe Pro Gly Thr Ala Thr
                    115                 120                 125

   20   ctt aca ccc gaa ggg aaa aaa gtt atg gga act gtt tta gcc gtt ctc   432
        Leu Thr Pro Glu Gly Lys Lys Val Met Gly Thr Val Leu Ala Val Leu
                130                 135                 140

        cgt gaa tat aat ctt tac ctt gtg ata cgt ggc cat gct gat att ggt   480
   25   Arg Glu Tyr Asn Leu Tyr Leu Val Ile Arg Gly His Ala Asp Ile Gly
        145                 150                 155                 160

        gaa ata aca aaa ggc agc cct ttt gct tct aac tgg gaa ctt tca gga   528
        Glu Ile Thr Lys Gly Ser Pro Phe Ala Ser Asn Trp Glu Leu Ser Gly
   30                       165                 170                 175

        gct cgt gca gct gca gct gca cag tat ctt gta gag cac ggg ata aag   576
        Ala Arg Ala Ala Ala Ala Ala Gln Tyr Leu Val Glu His Gly Ile Lys
                        180                 185                 190
   35
        gct tca cga att cgc tct gta gga tat gca gat aca aga cct cta gaa   624
        Ala Ser Arg Ile Arg Ser Val Gly Tyr Ala Asp Thr Arg Pro Leu Glu
                    195                 200                 205

   40   cct agt tct cct gaa gga agt aca aaa aat cgt cgt ata gaa ttc tat   672
        Pro Ser Ser Pro Glu Gly Ser Thr Lys Asn Arg Arg Ile Glu Phe Tyr
                210                 215                 220

        ttt cat cgg cca gaa gtt atg tct tat ggc gtt gta tat taa tag       717
   45   Phe His Arg Pro Glu Val Met Ser Tyr Gly Val Val Tyr
        225                 230                 235
```

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<210> 12
<211> 237
<212> PRT
<213> Lawsonia intracellularis

<400> 12
Met Ser Gly Ser Trp Lys Val Ala Tyr Ala Asp Phe Val Thr Ala Met
1               5               10                  15

Met Ala Phe Phe Leu Leu Met Trp Ile Leu Ala Met Thr Pro Pro Glu
            20              25                  30

Val Lys Glu Gly Leu Ala Ala Tyr Phe Ser Ser Ser Asp Ala Thr Phe
        35              40                  45

Lys Thr Pro Asp Ser Ser Pro Ile Ser Asn Asn Pro Leu Ile Asn Gln
        50              55                  60

Ile Asp Lys Leu Asp Thr Arg Gln Leu Lys Ile Asn Glu Thr Glu Gln
65              70                  75                      80

Ser His Tyr Ala Leu Ala Asn Lys Leu Lys Lys Met Leu Met Ala Asp
                85              90                  95

Ala Ile Pro Gln Ser Ala Thr Gly Ile Ser Ala Asp Asp Val Gly Val
            100             105                 110

Leu Leu Arg Val Asn Ser Asn Ser Thr Phe Phe Pro Gly Thr Ala Thr
        115             120                 125

Leu Thr Pro Glu Gly Lys Lys Val Met Gly Thr Val Leu Ala Val Leu
        130             135                 140

Arg Glu Tyr Asn Leu Tyr Leu Val Ile Arg Gly His Ala Asp Ile Gly
145             150                 155                     160

Glu Ile Thr Lys Gly Ser Pro Phe Ala Ser Asn Trp Glu Leu Ser Gly
                165             170                 175

Ala Arg Ala Ala Ala Ala Ala Gln Tyr Leu Val Glu His Gly Ile Lys
            180             185                 190

Ala Ser Arg Ile Arg Ser Val Gly Tyr Ala Asp Thr Arg Pro Leu Glu
        195             200                 205
```

```
      Pro Ser Ser Pro Glu Gly Ser Thr Lys Asn Arg Arg Ile Glu Phe Tyr
          210             215             220

 5    Phe His Arg Pro Glu Val Met Ser Tyr Gly Val Val Tyr
          225             230             235



      <210> 13
10    <211> 1047
      <212> DNA
      <213> Lawsonia intracellularis


      <220>
15    <221> CDS
      <222> (1)..(1044)


      <400> 13
      atg ata atc ctt tta gga act gtt ttt ctt att gtt ctt atc tct gca      48
20    Met Ile Ile Leu Leu Gly Thr Val Phe Leu Ile Val Leu Ile Ser Ala
       1               5                  10                  15


      tta tgc tca atg atg gaa gct gct ata tac tct atc cct att act tat      96
      Leu Cys Ser Met Met Glu Ala Ala Ile Tyr Ser Ile Pro Ile Thr Tyr
25               20                  25                  30


      att gaa cac ctt cgt gaa cag gga agc aaa aaa gga gaa aaa ctt tat     144
      Ile Glu His Leu Arg Glu Gln Gly Ser Lys Lys Gly Glu Lys Leu Tyr
                  35                  40                  45
30

      tat tta cat agt aat att gat cag cct att aca gcc gta tta ata ttg     192
      Tyr Leu His Ser Asn Ile Asp Gln Pro Ile Thr Ala Val Leu Ile Leu
          50                  55                  60


35    aat act ata gca aat act gct gga gct gcc ctt gct gga gca att gct     240
      Asn Thr Ile Ala Asn Thr Ala Gly Ala Ala Leu Ala Gly Ala Ile Ala
       65                  70                  75                  80


      aca aca aca ctt cat gaa tct act aag cct ttc ttt gca gca atc ctc     288
40    Thr Thr Thr Leu His Glu Ser Thr Lys Pro Phe Phe Ala Ala Ile Leu
                      85                  90                  95


      acc ttg ctt att tta gct ttt ggg gaa att ata cct aaa aca cta ggt     336
      Thr Leu Leu Ile Leu Ala Phe Gly Glu Ile Ile Pro Lys Thr Leu Gly
45                   100                 105                 110
```

- 20 -

```
        gtt gct tac tct aaa cgt att gct ata att ctc ctt aat cct ctc tct   384
        Val Ala Tyr Ser Lys Arg Ile Ala Ile Ile Leu Leu Asn Pro Leu Ser
                    115                 120                 125

  5     att ctt ata gtt act tta aaa ccc ctt att atg ctt tca agc tac tta   432
        Ile Leu Ile Val Thr Leu Lys Pro Leu Ile Met Leu Ser Ser Tyr Leu
                    130                 135                 140

        aca cga ctt gtt tca cct cga aaa cgt cct aca gtt aca gaa gat gac   480
 10     Thr Arg Leu Val Ser Pro Arg Lys Arg Pro Thr Val Thr Glu Asp Asp
        145                 150                 155                 160

        atc cgt gca ctt aca agt ctt tcc aga gag tct ggt cgt att aag cca   528
        Ile Arg Ala Leu Thr Ser Leu Ser Arg Glu Ser Gly Arg Ile Lys Pro
 15                     165                 170                 175

        tat gaa gaa cat gtc ata aaa aat atc ctt agt ctt gat tta aaa tat   576
        Tyr Glu Glu His Val Ile Lys Asn Ile Leu Ser Leu Asp Leu Lys Tyr
                        180                 185                 190
 20
        gct cat gaa att atg act ccc aga act atg gtc ttt tca ctt cat gaa   624
        Ala His Glu Ile Met Thr Pro Arg Thr Met Val Phe Ser Leu His Glu
                    195                 200                 205

 25     aac ctt act gtc tct gaa gct tat agc aac ccc aaa ata tgg aac tat   672
        Asn Leu Thr Val Ser Glu Ala Tyr Ser Asn Pro Lys Ile Trp Asn Tyr
                    210                 215                 220

        agt cgc atc cct act tat gga gaa aat aac gaa gac att act ggc att   720
 30     Ser Arg Ile Pro Thr Tyr Gly Glu Asn Asn Glu Asp Ile Thr Gly Ile
        225                 230                 235                 240

        atc caa cga tat gaa att gga cga tat atg acc aat gga gaa aca gaa   768
        Ile Gln Arg Tyr Glu Ile Gly Arg Tyr Met Thr Asn Gly Glu Thr Glu
 35                     245                 250                 255

        aaa aaa ctt tta gaa att atg caa cca gca aaa ttt gtc ctt gaa agt   816
        Lys Lys Leu Leu Glu Ile Met Gln Pro Ala Lys Phe Val Leu Glu Ser
                    260                 265                 270
 40
        caa act gta gat cat tta ctt ctt gca ttt tta gaa gaa aga caa cat   864
        Gln Thr Val Asp His Leu Leu Leu Ala Phe Leu Glu Glu Arg Gln His
                    275                 280                 285

 45     ctt ttt att gta ctt gat gag tat ggg gga tta tct ggt gtt gtt tcc   912
        Leu Phe Ile Val Leu Asp Glu Tyr Gly Gly Leu Ser Gly Val Val Ser
```

```
              290                    295                    300

     tta gaa gat gta tta gaa act atg ctt gga aga gaa att gtt gat gaa   960
     Leu Glu Asp Val Leu Glu Thr Met Leu Gly Arg Glu Ile Val Asp Glu
 5   305                    310                    315                    320


     agt gat aca aca cct gat ctt aga gca ctt gca aaa aaa aga cat agt   1008
     Ser Asp Thr Thr Pro Asp Leu Arg Ala Leu Ala Lys Lys Arg His Ser
                        325                    330                    335
10

     gca tta atc caa aat aat aaa aat act ctt tta aaa taa             1047
     Ala Leu Ile Gln Asn Asn Lys Asn Thr Leu Leu Lys
                        340               ˎ       345


15

     <210> 14
     <211> 348
     <212> PRT
     <213> Lawsonia intracellularis

20
     <400> 14
     Met Ile Ile Leu Leu Gly Thr Val Phe Leu Ile Val Leu Ile Ser Ala
      1               5                   10                  15


25   Leu Cys Ser Met Met Glu Ala Ala Ile Tyr Ser Ile Pro Ile Thr Tyr
                     20                  25                  30


     Ile Glu His Leu Arg Glu Gln Gly Ser Lys Lys Gly Glu Lys Leu Tyr
                 35                  40                  45
30

     Tyr Leu His Ser Asn Ile Asp Gln Pro Ile Thr Ala Val Leu Ile Leu
             50                  55                  60


     Asn Thr Ile Ala Asn Thr Ala Gly Ala Ala Leu Ala Gly Ala Ile Ala
35   65                  70                  75                  80


     Thr Thr Thr Leu His Glu Ser Thr Lys Pro Phe Phe Ala Ala Ile Leu
                     85                  90                  95


40   Thr Leu Leu Ile Leu Ala Phe Gly Glu Ile Ile Pro Lys Thr Leu Gly
                     100                 105                 110


     Val Ala Tyr Ser Lys Arg Ile Ala Ile Ile Leu Leu Asn Pro Leu Ser
                 115                 120                 125
45

     Ile Leu Ile Val Thr Leu Lys Pro Leu Ile Met Leu Ser Ser Tyr Leu
```

```
                  130                 135                 140

        Thr Arg Leu Val Ser Pro Arg Lys Arg Pro Thr Val Thr Glu Asp Asp
        145                 150                 155                 160
 5

        Ile Arg Ala Leu Thr Ser Leu Ser Arg Glu Ser Gly Arg Ile Lys Pro
                        165                 170                 175

        Tyr Glu Glu His Val Ile Lys Asn Ile Leu Ser Leu Asp Leu Lys Tyr
10                      180                 185                 190

        Ala His Glu Ile Met Thr Pro Arg Thr Met Val Phe Ser Leu His Glu
                        195                 200                 205

15      Asn Leu Thr Val Ser Glu Ala Tyr Ser Asn Pro Lys Ile Trp Asn Tyr
                210                 215                 220

        Ser Arg Ile Pro Thr Tyr Gly Glu Asn Asn Glu Asp Ile Thr Gly Ile
        225                 230                 235                 240
20

        Ile Gln Arg Tyr Glu Ile Gly Arg Tyr Met Thr Asn Gly Glu Thr Glu
                        245                 250                 255

        Lys Lys Leu Leu Glu Ile Met Gln Pro Ala Lys Phe Val Leu Glu Ser
25                      260                 265                 270

        Gln Thr Val Asp His Leu Leu Leu Ala Phe Leu Glu Glu Arg Gln His
                        275                 280                 285

30      Leu Phe Ile Val Leu Asp Glu Tyr Gly Gly Leu Ser Gly Val Val Ser
                290                 295                 300

        Leu Glu Asp Val Leu Glu Thr Met Leu Gly Arg Glu Ile Val Asp Glu
        305                 310                 315                 320
35

        Ser Asp Thr Thr Pro Asp Leu Arg Ala Leu Ala Lys Lys Arg His Ser
                        325                 330                 335

        Ala Leu Ile Gln Asn Asn Lys Asn Thr Leu Leu Lys
40                      340                 345


        <210> 15
        <211> 1812
45      <212> DNA
        <213> Lawsonia intracellularis
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- 23 -

<220>
<221> CDS
<222> (1)..(1809)

5

<400> 15

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atg caa aaa gta tgt tat ttt ttt ctt ata acc ttt ttc tac ttt ttc    48
Met Gln Lys Val Cys Tyr Phe Phe Leu Ile Thr Phe Phe Tyr Phe Phe
 1               5                  10                  15
```

10

```
ata aca gaa aat tat ctc ttt gct aca tca att acc act tcc aca att    96
Ile Thr Glu Asn Tyr Leu Phe Ala Thr Ser Ile Thr Thr Ser Thr Ile
                20                  25                  30
```

15

```
aac caa caa cat ata gca tat aca gtt act ttt acc tct cca gaa aat   144
Asn Gln Gln His Ile Ala Tyr Thr Val Thr Phe Thr Ser Pro Glu Asn
            35                  40                  45
```

```
cct aat ctt gca aca gag atg gaa aca cat agt gaa tta gta aag ctt   192
Pro Asn Leu Ala Thr Glu Met Glu Thr His Ser Glu Leu Val Lys Leu
20          50                  55                  60
```

```
gca aat caa tct tta gat agt aaa ata ggt tta aat tta cgt gtt aaa   240
Ala Asn Gln Ser Leu Asp Ser Lys Ile Gly Leu Asn Leu Arg Val Lys
25      65                  70                  75                  80
```

```
gaa gat ata agt aca gca caa aaa att ctt gac tcg aat ggt tat tat   288
Glu Asp Ile Ser Thr Ala Gln Lys Ile Leu Asp Ser Asn Gly Tyr Tyr
                        85                  90                  95
```

30

```
agt gga agt gtc gag gga aag att gac tgg cag acg aac cct att agt   336
Ser Gly Ser Val Glu Gly Lys Ile Asp Trp Gln Thr Asn Pro Ile Ser
                100                 105                 110
```

35

```
atc caa atc caa ttt aaa cca aat gta caa tat aaa ata aat aca ata   384
Ile Gln Ile Gln Phe Lys Pro Asn Val Gln Tyr Lys Ile Asn Thr Ile
            115                 120                 125
```

```
cat atc caa tac ctt gat agt gaa ctt gca tat ctc cct ctt tcc tta   432
His Ile Gln Tyr Leu Asp Ser Glu Leu Ala Tyr Leu Pro Leu Ser Leu
40          130                 135                 140
```

```
gaa gaa ttc aat ctc tct aaa ggt aat cct gct ctt gct gtt aat atc   480
Glu Glu Phe Asn Leu Ser Lys Gly Asn Pro Ala Leu Ala Val Asn Ile
45  145                 150                 155                 160
```

- 24 -

```
cta tcc tct gta agt agc ctc atg caa tat ata cat aat aat gga tat    528
Leu Ser Ser Val Ser Ser Leu Met Gln Tyr Ile His Asn Asn Gly Tyr
                165             170             175
```

```
cca tta gcc aaa ata aaa aaa act caa tac ata att aat cgg atg gat    576
Pro Leu Ala Lys Ile Lys Lys Thr Gln Tyr Ile Ile Asn Arg Met Asp
            180             185             190
```

```
tat aca ttt gat att gat tta gta ata aga caa gga ccg tta ctc cat    624
Tyr Thr Phe Asp Ile Asp Leu Val Ile Arg Gln Gly Pro Leu Leu His
            195             200             205
```

```
atg ggt aaa gta caa cct caa cat aat ctc aat att tca aca ata ttc    672
Met Gly Lys Val Gln Pro Gln His Asn Leu Asn Ile Ser Thr Ile Phe
            210             215             220
```

```
cta aat aaa att gct aca tgg aag gaa gga agg gta tgg aac aat gca    720
Leu Asn Lys Ile Ala Thr Trp Lys Glu Gly Arg Val Trp Asn Asn Ala
225             230             235             240
```

```
ctc ctt gat tct tat cga aca cgg ctt caa caa aca ggc ctt ttc agt    768
Leu Leu Asp Ser Tyr Arg Thr Arg Leu Gln Gln Thr Gly Leu Phe Ser
                245             250             255
```

```
tct ata act ctc aat cca agg aat caa aaa gaa caa aat ggt aac acc    816
Ser Ile Thr Leu Asn Pro Arg Asn Gln Lys Glu Gln Asn Gly Asn Thr
                260             265             270
```

```
tct ata gaa ctt gtt gca aca gaa gcc cct cca agg act att agt ggt    864
Ser Ile Glu Leu Val Ala Thr Glu Ala Pro Pro Arg Thr Ile Ser Gly
            275             280             285
```

```
ggc tta caa tac tct tct gat caa ggt att ggt gca cgt ggg act tgg    912
Gly Leu Gln Tyr Ser Ser Asp Gln Gly Ile Gly Ala Arg Gly Thr Trp
            290             295             300
```

```
gaa cat cga aat gtt ttt ggt aat gga gaa ctt ttt cgt ata aca gca    960
Glu His Arg Asn Val Phe Gly Asn Gly Glu Leu Phe Arg Ile Thr Ala
305             310             315             320
```

```
cca ata agt cga gat gat caa aaa att atg gca aac ttc caa aaa cca    1008
Pro Ile Ser Arg Asp Asp Gln Lys Ile Met Ala Asn Phe Gln Lys Pro
                325             330             335
```

```
gcc ttt ggc cgt cca aat caa tca tta att agt gaa gca caa ctt aaa    1056
Ala Phe Gly Arg Pro Asn Gln Ser Leu Ile Ser Glu Ala Gln Leu Lys
```

```
                    340                 345                 350

      aaa gaa aat aca aaa agt tac aaa caa caa ctt gca tct att gct tta    1104
      Lys Glu Asn Thr Lys Ser Tyr Lys Gln Gln Leu Ala Ser Ile Ala Leu
 5            355                 360                 365

      gga att gaa cga caa ttt aat aga cgt tgg ttt ggt agt agc agt ctt    1152
      Gly Ile Glu Arg Gln Phe Asn Arg Arg Trp Phe Gly Ser Ser Ser Leu
             370                 375                 380
10
      tca gtt gat aca gga ttt atg gat gat cga gat tct ata aaa aaa ata    1200
      Ser Val Asp Thr Gly Phe Met Asp Asp Arg Asp Ser Ile Lys Lys Ile
      385                 390                 395                 400

15    ttt act ctt ttt ggc atc ccc tta tca ata aca agg gat agt tct aaa    1248
      Phe Thr Leu Phe Gly Ile Pro Leu Ser Ile Thr Arg Asp Ser Ser Lys
                     405                 410                 415

      gat cct ctt aat cct atc caa gga aca aaa gct acc tta aat gtt act    1296
20    Asp Pro Leu Asn Pro Ile Gln Gly Thr Lys Ala Thr Leu Asn Val Thr
                     420                 425                 430

      cct tat att ggt aaa tat aaa aaa aag att ttg act tta cgt agt cgg    1344
      Pro Tyr Ile Gly Lys Tyr Lys Lys Lys Ile Leu Thr Leu Arg Ser Arg
25            435                 440                 445

      ttt gat ttt agc ttt tac ata gac gtt ctt aaa aca ggg aaa ctt atc    1392
      Phe Asp Phe Ser Phe Tyr Ile Asp Val Leu Lys Thr Gly Lys Leu Ile
             450                 455                 460
30
      ttg gct aac aaa ata gca ata ggt tcc ctc cta ggg aaa gat ata gaa    1440
      Leu Ala Asn Lys Ile Ala Ile Gly Ser Leu Leu Gly Lys Asp Ile Glu
      465                 470                 475                 480

35    aac tat cct gca ata cta agg ttt tat gct ggg ggt ggt ggt agt gta    1488
      Asn Tyr Pro Ala Ile Leu Arg Phe Tyr Ala Gly Gly Gly Gly Ser Val
                     485                 490                 495

      aga ggg tat gac tat caa tca ttg gga cca aaa aat aaa tat ggg gat    1536
40    Arg Gly Tyr Asp Tyr Gln Ser Leu Gly Pro Lys Asn Lys Tyr Gly Asp
                     500                 505                 510

      gct att gga gga ctt tct ttt tca act att agt ttt gaa tta cga tta    1584
      Ala Ile Gly Gly Leu Ser Phe Ser Thr Ile Ser Phe Glu Leu Arg Leu
45            515                 520                 525
```

```
aaa ata aca gaa tcc att ggc att gtg cca att tat tgg atg ggg gaa    1632
Lys Ile Thr Glu Ser Ile Gly Ile Val Pro Ile Tyr Trp Met Gly Glu
        530                 535                 540


tat tta cga aaa aaa aat ttc ctg act tta aaa aaa tca ata tat tgg    1680
Tyr Leu Arg Lys Lys Asn Phe Leu Thr Leu Lys Lys Ser Ile Tyr Trp
545                 550                 555                 560


ggg gta ggc ctg ggg cta cga tat tat aca agt ttt gcc ccc ata cgt    1728
Gly Val Gly Leu Gly Leu Arg Tyr Tyr Thr Ser Phe Ala Pro Ile Arg
                565                 570                 575


tta gat ata gca act cca ctt caa gat aga agc cat aat aaa cac ttt    1776
Leu Asp Ile Ala Thr Pro Leu Gln Asp Arg Ser His Asn Lys His Phe
                580                 585                 590


caa ctt tat att agt att ggg caa gca ttc taa tga                    1812
Gln Leu Tyr Ile Ser Ile Gly Gln Ala Phe
                595                 600



<210> 16
<211> 602
<212> PRT
<213> Lawsonia intracellularis


<400> 16
Met Gln Lys Val Cys Tyr Phe Phe Leu Ile Thr Phe Phe Tyr Phe Phe
  1                 5                  10                  15


Ile Thr Glu Asn Tyr Leu Phe Ala Thr Ser Ile Thr Thr Ser Thr Ile
                20                  25                  30


Asn Gln Gln His Ile Ala Tyr Thr Val Thr Phe Thr Ser Pro Glu Asn
            35                  40                  45


Pro Asn Leu Ala Thr Glu Met Glu Thr His Ser Glu Leu Val Lys Leu
        50                  55                  60


Ala Asn Gln Ser Leu Asp Ser Lys Ile Gly Leu Asn Leu Arg Val Lys
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Glu Asp Ile Ser Thr Ala Gln Lys Ile Leu Asp Ser Asn Gly Tyr Tyr
                85                  90                  95


Ser Gly Ser Val Glu Gly Lys Ile Asp Trp Gln Thr Asn Pro Ile Ser
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                    100                 105                 110

      Ile Gln Ile Gln Phe Lys Pro Asn Val Gln Tyr Lys Ile Asn Thr Ile
               115                 120                 125
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      His Ile Gln Tyr Leu Asp Ser Glu Leu Ala Tyr Leu Pro Leu Ser Leu
               130                 135                 140

      Glu Glu Phe Asn Leu Ser Lys Gly Asn Pro Ala Leu Ala Val Asn Ile
10    145                 150                 155                 160

      Leu Ser Ser Val Ser Ser Leu Met Gln Tyr Ile His Asn Asn Gly Tyr
                         165                 170                 175

15    Pro Leu Ala Lys Ile Lys Lys Thr Gln Tyr Ile Ile Asn Arg Met Asp
                    180                 185                 190

      Tyr Thr Phe Asp Ile Asp Leu Val Ile Arg Gln Gly Pro Leu Leu His
                    195                 200                 205
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      Met Gly Lys Val Gln Pro Gln His Asn Leu Asn Ile Ser Thr Ile Phe
               210                 215                 220

      Leu Asn Lys Ile Ala Thr Trp Lys Glu Gly Arg Val Trp Asn Asn Ala
25    225                 230                 235                 240

      Leu Leu Asp Ser Tyr Arg Thr Arg Leu Gln Gln Thr Gly Leu Phe Ser
                    245                 250                 255

30    Ser Ile Thr Leu Asn Pro Arg Asn Gln Lys Glu Gln Asn Gly Asn Thr
                    260                 265                 270

      Ser Ile Glu Leu Val Ala Thr Glu Ala Pro Pro Arg Thr Ile Ser Gly
                    275                 280                 285
35

      Gly Leu Gln Tyr Ser Ser Asp Gln Gly Ile Gly Ala Arg Gly Thr Trp
                    290                 295                 300

      Glu His Arg Asn Val Phe Gly Asn Gly Glu Leu Phe Arg Ile Thr Ala
40    305                 310                 315                 320

      Pro Ile Ser Arg Asp Asp Gln Lys Ile Met Ala Asn Phe Gln Lys Pro
                    325                 330                 335

45    Ala Phe Gly Arg Pro Asn Gln Ser Leu Ile Ser Glu Ala Gln Leu Lys
                    340                 345                 350
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       Lys Glu Asn Thr Lys Ser Tyr Lys Gln Gln Leu Ala Ser Ile Ala Leu
               355                 360                 365

  5    Gly Ile Glu Arg Gln Phe Asn Arg Arg Trp Phe Gly Ser Ser Ser Leu
               370                 375                 380

       Ser Val Asp Thr Gly Phe Met Asp Asp Arg Asp Ser Ile Lys Lys Ile
       385                 390                 395                 400
 10
       Phe Thr Leu Phe Gly Ile Pro Leu Ser Ile Thr Arg Asp Ser Ser Lys
                       405                 410                 415

       Asp Pro Leu Asn Pro Ile Gln Gly Thr Lys Ala Thr Leu Asn Val Thr
 15                420                 425                 430

       Pro Tyr Ile Gly Lys Tyr Lys Lys Lys Ile Leu Thr Leu Arg Ser Arg
                   435                 440                 445

 20    Phe Asp Phe Ser Phe Tyr Ile Asp Val Leu Lys Thr Gly Lys Leu Ile
               450                 455                 460

       Leu Ala Asn Lys Ile Ala Ile Gly Ser Leu Leu Gly Lys Asp Ile Glu
       465                 470                 475                 480
 25
       Asn Tyr Pro Ala Ile Leu Arg Phe Tyr Ala Gly Gly Gly Gly Ser Val
                       485                 490                 495

       Arg Gly Tyr Asp Tyr Gln Ser Leu Gly Pro Lys Asn Lys Tyr Gly Asp
 30                500                 505                 510

       Ala Ile Gly Gly Leu Ser Phe Ser Thr Ile Ser Phe Glu Leu Arg Leu
                   515                 520                 525

 35    Lys Ile Thr Glu Ser Ile Gly Ile Val Pro Ile Tyr Trp Met Gly Glu
               530                 535                 540

       Tyr Leu Arg Lys Lys Asn Phe Leu Thr Leu Lys Lys Ser Ile Tyr Trp
       545                 550                 555                 560
 40
       Gly Val Gly Leu Gly Leu Arg Tyr Tyr Thr Ser Phe Ala Pro Ile Arg
                   565                 570                 575

       Leu Asp Ile Ala Thr Pro Leu Gln Asp Arg Ser His Asn Lys His Phe
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          1               5                  10                  15


        gca ttt acg tta ttt tta gga ctt att att aca ggc att ctt ttt ata     96
        Ala Phe Thr Leu Phe Leu Gly Leu Ile Ile Thr Gly Ile Leu Phe Ile
 20                 20                  25                  30


        cgg acc tct aca ggc att gct tgg att aaa aat aca gtt tct tct tta    144
        Arg Thr Ser Thr Gly Ile Ala Trp Ile Lys Asn Thr Val Ser Ser Leu
                35                  40                  45
 25
        ctt caa caa caa gga att ata cta caa gta tct tca att att gga cca    192
        Leu Gln Gln Gln Gly Ile Ile Leu Gln Val Ser Ser Ile Ile Gly Pro
                50                  55                  60


 30     ttc cca gaa caa att act att aat gaa ctt agc ctt agt gat gtg aat    240
        Phe Pro Glu Gln Ile Thr Ile Asn Glu Leu Ser Leu Ser Asp Val Asn
         65                  70                  75                  80


        gga act tac ctt aca ata tct aac tta gaa atc caa tca aac tta tgg    288
 35     Gly Thr Tyr Leu Thr Ile Ser Asn Leu Glu Ile Gln Ser Asn Leu Trp
                        85                  90                  95


        gct tta ttc aaa ggt caa ctt gaa att ctg tct ttt gaa ctt aat gat    336
        Ala Leu Phe Lys Gly Gln Leu Glu Ile Leu Ser Phe Glu Leu Asn Asp
 40                100                 105                 110


        ctt gta tta tat cgc tta ccc tca aat aat aat cta aaa aaa tca tct    384
        Leu Val Leu Tyr Arg Leu Pro Ser Asn Asn Asn Leu Lys Lys Ser Ser
                115                 120                 125
 45
        aca agt ttt gtg tta cct cac ata tca ttt gat tta act cca tgg tgg    432
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- 30 -

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        Thr Ser Phe Val Leu Pro His Ile Ser Phe Asp Leu Thr Pro Trp Trp
            130                 135                 140


        act gaa cat att cgt att caa aac atc cat att aac aat aca caa ctt   480
   5    Thr Glu His Ile Arg Ile Gln Asn Ile His Ile Asn Asn Thr Gln Leu
        145                 150                 155                 160


        tcc tct gat att ata ggt att cca ttg gta tta tcc ctt gag ggt gat   528
        Ser Ser Asp Ile Ile Gly Ile Pro Leu Val Leu Ser Leu Glu Gly Asp
  10                    165                 170                 175


        ggt aca tta aca aat tgg aat gga aca ttt caa cta tcc tct tct aac   576
        Gly Thr Leu Thr Asn Trp Asn Gly Thr Phe Gln Leu Ser Ser Ser Asn
                    180                 185                 190
  15

        aaa aca aaa att ata gga acg ctt cgt tac caa ggg aat aag aca caa   624
        Lys Thr Lys Ile Ile Gly Thr Leu Arg Tyr Gln Gly Asn Lys Thr Gln
                    195                 200                 205


  20    ttt ttt gaa tat gtt cat cct aca cgg ata gta aca cta gag ata gac   672
        Phe Phe Glu Tyr Val His Pro Thr Arg Ile Val Thr Leu Glu Ile Asp
            210                 215                 220


        agc gta gct gat aaa aag tca tat aat aat agt atc ctt gaa caa cct   720
  25    Ser Val Ala Asp Lys Lys Ser Tyr Asn Asn Ser Ile Leu Glu Gln Pro
        225                 230                 235                 240


        cta cat tta cac ctt tct att tat cct gaa cat aat aga att atc tta   768
        Leu His Leu His Leu Ser Ile Tyr Pro Glu His Asn Arg Ile Ile Leu
  30                    245                 250                 255


        cac tca tta cta gct gaa tat ggt agc tgg tta ctt aca tca gaa agt   816
        His Ser Leu Leu Ala Glu Tyr Gly Ser Trp Leu Leu Thr Ser Glu Ser
                    260                 265                 270
  35

        att gaa gta tct aat gag caa tta aaa gga aat att tta tta aaa tat   864
        Ile Glu Val Ser Asn Glu Gln Leu Lys Gly Asn Ile Leu Leu Lys Tyr
                    275                 280                 285


  40    aat gga gaa gct act cat caa ctt cct ata aaa aaa ctt aac tca tca   912
        Asn Gly Glu Ala Thr His Gln Leu Pro Ile Lys Lys Leu Asn Ser Ser
            290                 295                 300


        att acc ctc agt ggc tca cta aat aaa cct aat ttt agt ata caa atg   960
  45    Ile Thr Leu Ser Gly Ser Leu Asn Lys Pro Asn Phe Ser Ile Gln Met
        305                 310                 315                 320
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        aca tta cct gaa att aac att aca aaa aac ata ata gat ctt caa aca   1008
        Thr Leu Pro Glu Ile Asn Ile Thr Lys Asn Ile Ile Asp Leu Gln Thr
                     325             330             335
  5

        gaa ctt gtt att aat cta gga ctt ttc tct act cac tct gat att ctt   1056
        Glu Leu Val Ile Asn Leu Gly Leu Phe Ser Thr His Ser Asp Ile Leu
                     340             345             350

 10     aca tct ggg aca att aca gta cag gga gaa act ata ccc aat agt att   1104
        Thr Ser Gly Thr Ile Thr Val Gln Gly Glu Thr Ile Pro Asn Ser Ile
                     355             360             365

        ctt tcc agt gca gtt gat ata ata gcc tct aca aca aca cat aca att   1152
 15     Leu Ser Ser Ala Val Asp Ile Ile Ala Ser Thr Thr Thr His Thr Ile
                     370             375             380

        acc tta gag cat gca acc tta aca tct cca gaa atg cat ttt tcc cta   1200
        Thr Leu Glu His Ala Thr Leu Thr Ser Pro Glu Met His Phe Ser Leu
 20     385             390             395             400

        tct gga gaa ttt aat agt ctt cta gga aat atc gat gca aac cta aaa   1248
        Ser Gly Glu Phe Asn Ser Leu Leu Gly Asn Ile Asp Ala Asn Leu Lys
                     405             410             415
 25
        ggt aat act cca act ctt agt ata ttt tct tct ctt ctt gga cta cct   1296
        Gly Asn Thr Pro Thr Leu Ser Ile Phe Ser Ser Leu Leu Gly Leu Pro
                     420             425             430

 30     gat ctt act ggg caa agt aac att act ata gga tta cac cgt caa ggg   1344
        Asp Leu Thr Gly Gln Ser Asn Ile Thr Ile Gly Leu His Arg Gln Gly
                     435             440             445

        tct tcc tct tca ata gaa gga aca gca act gtc tca ctt aat aat atg   1392
 35     Ser Ser Ser Ser Ile Glu Gly Thr Ala Thr Val Ser Leu Asn Asn Met
                     450             455             460

        aac tgg gga gta caa gca tta cag ggg aca tta ggt gat aat gca act   1440
        Asn Trp Gly Val Gln Ala Leu Gln Gly Thr Leu Gly Asp Asn Ala Thr
 40     465             470             475             480

        cta agt gga ata tat aat tta act ccc ata gac tgg tct att tct tta   1488
        Leu Ser Gly Ile Tyr Asn Leu Thr Pro Ile Asp Trp Ser Ile Ser Leu
                     485             490             495
 45
        aac aaa ttg aaa tta aca gca aag aat gtt tat gct gaa ggc ctt att   1536
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        Asn Lys Leu Lys Leu Thr Ala Lys Asn Val Tyr Ala Glu Gly Leu Ile
                500                 505                 510

        aat ttt caa aaa aaa tac ata gat agc tct ata aat ctt ata att cct   1584
   5    Asn Phe Gln Lys Lys Tyr Ile Asp Ser Ser Ile Asn Leu Ile Ile Pro
                515                 520                 525

        aac ctt cag cta ata gct cct cct ata tct gga gag tta caa tcc tta   1632
        Asn Leu Gln Leu Ile Ala Pro Pro Ile Ser Gly Glu Leu Gln Ser Leu
  10        530                 535                 540

        att aca gtg tct gga aaa ctt gac gca cct tct ata gaa agc aaa att   1680
        Ile Thr Val Ser Gly Lys Leu Asp Ala Pro Ser Ile Glu Ser Lys Ile
        545                 550                 555                 560
  15
        ttt tca tca caa ctc acc tgg aat gcg ctc caa ctt aat aat cct caa   1728
        Phe Ser Ser Gln Leu Thr Trp Asn Ala Leu Gln Leu Asn Asn Pro Gln
                        565                 570                 575

  20    ctc ata ata act act act caa tct tct tcc tct gcg att aaa ggt aat   1776
        Leu Ile Ile Thr Thr Thr Gln Ser Ser Ser Ser Ala Ile Lys Gly Asn
                        580                 585                 590

        ata aca ctc tcg gct gag cca gct tca tct gag gca tta acc ttt tca   1824
  25    Ile Thr Leu Ser Ala Glu Pro Ala Ser Ser Glu Ala Leu Thr Phe Ser
                    595                 600                 605

        agt aat tgg gga atc cta cct acg gaa ata cta gta gaa aaa att ata   1872
        Ser Asn Trp Gly Ile Leu Pro Thr Glu Ile Leu Val Glu Lys Ile Ile
  30        610                 615                 620

        gga aat ata tta gga gta aat ctt gat ggt aat att aaa ata aca aaa   1920
        Gly Asn Ile Leu Gly Val Asn Leu Asp Gly Asn Ile Lys Ile Thr Lys
        625                 630                 635                 640
  35
        aaa gat tac ctt ata aat ggt gat att att gca gaa gtt cag tct tgg   1968
        Lys Asp Tyr Leu Ile Asn Gly Asp Ile Ile Ala Glu Val Gln Ser Trp
                        645                 650                 655

  40    aaa gat att gca aac ata ttg caa ata cct att aga ggt tca gca tca   2016
        Lys Asp Ile Ala Asn Ile Leu Gln Ile Pro Ile Arg Gly Ser Ala Ser
                        660                 665                 670

        ata aaa ata cag ttt gat cca aag aat caa caa tgt att tct act caa   2064
  45    Ile Lys Ile Gln Phe Asp Pro Lys Asn Gln Gln Cys Ile Ser Thr Gln
                675                 680                 685
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     tgg caa tta aaa aat ttc ata tta ggt aat aat ttt aat gta act act    2112
     Trp Gln Leu Lys Asn Phe Ile Leu Gly Asn Asn Phe Asn Val Thr Thr
         690             695             700
 5

     ata aaa gga aga gca gat aca ata caa ctt cat aag aat cct aca att    2160
     Ile Lys Gly Arg Ala Asp Thr Ile Gln Leu His Lys Asn Pro Thr Ile
     705             710             715             720

10   gct ctc tct tca aaa att ggt gct ggt aca tat gaa gac ttt caa tgg    2208
     Ala Leu Ser Ser Lys Ile Gly Ala Gly Thr Tyr Glu Asp Phe Gln Trp
                     725             730             735

     aca caa ggg acg tta gac ata aaa ggc aca tta aaa aat ttt aat agt    2256
15   Thr Gln Gly Thr Leu Asp Ile Lys Gly Thr Leu Lys Asn Phe Asn Ser
                 740             745             750

     aaa ata aat ata gca gga caa aca act gta aac gca aac ttt caa aca    2304
     Lys Ile Asn Ile Ala Gly Gln Thr Thr Val Asn Ala Asn Phe Gln Thr
20           755             760             765

     aat ctt ttt gaa aaa aat att aat ata act act ctt aat tta aaa aat    2352
     Asn Leu Phe Glu Lys Asn Ile Asn Ile Thr Thr Leu Asn Leu Lys Asn
         770             775             780
25

     att caa aaa aat ata gga att aag ctc ctt cag cca ata aaa att ata    2400
     Ile Gln Lys Asn Ile Gly Ile Lys Leu Leu Gln Pro Ile Lys Ile Ile
     785             790             795             800

30   gtc tca cct caa caa ttt gtt ctt aat aac tgt tca cta gca att ctt    2448
     Val Ser Pro Gln Gln Phe Val Leu Asn Asn Cys Ser Leu Ala Ile Leu
                     805             810             815

     cca tct gga aca att aca act gat ata tat gtt act cct caa cga ctt    2496
35   Pro Ser Gly Thr Ile Thr Thr Asp Ile Tyr Val Thr Pro Gln Arg Leu
                 820             825             830

     aat gct aat gca atc att aaa gaa gtt tca ctt ctc tct ttc caa cca    2544
     Asn Ala Asn Ala Ile Ile Lys Glu Val Ser Leu Leu Ser Phe Gln Pro
40           835             840             845

     ttt agt ata ctt ctt cct caa gga aat ata aat gga cac ata aca ctt    2592
     Phe Ser Ile Leu Leu Pro Gln Gly Asn Ile Asn Gly His Ile Thr Leu
         850             855             860
45

     aca gga ata cct agt aaa cct aaa gga aca ctc tca ttt gat att cta    2640
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        Thr Gly Ile Pro Ser Lys Pro Lys Gly Thr Leu Ser Phe Asp Ile Leu
        865             870             875             880


        aac ata cat tat cca agg cca aat cca tca ata gca aac tta cat gta    2688
 5      Asn Ile His Tyr Pro Arg Pro Asn Pro Ser Ile Ala Asn Leu His Val
                        885             890             895


        gaa ggg gaa att ata tct tct cct aac aat ata tgt aaa ctt aat gca    2736
        Glu Gly Glu Ile Ile Ser Ser Pro Asn Asn Ile Cys Lys Leu Asn Ala
10                      900             905             910


        acc cta aca gaa aaa aaa gag cct ata cct ata tca ata caa gca aca    2784
        Thr Leu Thr Glu Lys Lys Glu Pro Ile Pro Ile Ser Ile Gln Ala Thr
                        915             920             925
15

        ctc cct ttt gag ttc aca gaa aac aat atc cct atg cta tct aaa atg    2832
        Leu Pro Phe Glu Phe Thr Glu Asn Asn Ile Pro Met Leu Ser Lys Met
                930             935             940

20      agg cct ttt tct gcc cat atc aag tgg act gga ata tta gat aca ctt    2880
        Arg Pro Phe Ser Ala His Ile Lys Trp Thr Gly Ile Leu Asp Thr Leu
        945             950             955             960


        tgg aaa ctc att cca ctt act gat tac att atg gct ggg aat gga tct    2928
25      Trp Lys Leu Ile Pro Leu Thr Asp Tyr Ile Met Ala Gly Asn Gly Ser
                        965             970             975


        tta gat gct tct ctt tct ggg act tta gat agt cca aca tat gca att    2976
        Leu Asp Ala Ser Leu Ser Gly Thr Leu Asp Ser Pro Thr Tyr Ala Ile
30                      980             985             990


        ata aca aca ctt tct aat gct aac ttt caa gat ctc tcc ctt ggt ctt    3024
        Ile Thr Thr Leu Ser Asn Ala Asn Phe Gln Asp Leu Ser Leu Gly Leu
                995             1000            1005
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        tac tta gaa aat atc aat gct aaa tta cag gtc ttt tct aat aga atc    3072
        Tyr Leu Glu Asn Ile Asn Ala Lys Leu Gln Val Phe Ser Asn Arg Ile
            1010            1015            1020


40      tcc cat att caa gct aca gca tct gat ggt aaa caa ggt agt ata caa    3120
        Ser His Ile Gln Ala Thr Ala Ser Asp Gly Lys Gln Gly Ser Ile Gln
        1025            1030            1035            1040


        ctt att ggt aat att ggc tca tct aaa gaa cac ttt cct ttg tct att    3168
45      Leu Ile Gly Asn Ile Gly Ser Ser Lys Glu His Phe Pro Leu Ser Ile
                        1045            1050            1055
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      aat ggc tcc ttt aca aac ctt gct cca tta caa cgt aaa gac cta agt    3216
      Asn Gly Ser Phe Thr Asn Leu Ala Pro Leu Gln Arg Lys Asp Leu Ser
                  1060            1065                1070
  5

      ctt aca ctt tca gga gca gct act ctt gaa gga aca tta aaa cag tct    3264
      Leu Thr Leu Ser Gly Ala Ala Thr Leu Glu Gly Thr Leu Lys Gln Ser
              1075                1080                1085

 10   gaa gtt aaa ggc gat att gtt att aac caa ggc gaa ttt caa ctt act    3312
      Glu Val Lys Gly Asp Ile Val Ile Asn Gln Gly Glu Phe Gln Leu Thr
          1090                1095                1100

      gaa ggg tta acc agt aat att cca act ctt aat gta gtt gat agc act    3360
 15   Glu Gly Leu Thr Ser Asn Ile Pro Thr Leu Asn Val Val Asp Ser Thr
      1105                1110                1115                1120

      caa caa caa aat aca aag acc aaa aaa gct acc tat caa caa cct acc    3408
      Gln Gln Gln Asn Thr Lys Thr Lys Lys Ala Thr Tyr Gln Gln Pro Thr
 20               1125                1130                1135

      tta tct att gcg tta agt atc ccg aat cgt ttt ttt gtc cgt agt agt    3456
      Leu Ser Ile Ala Leu Ser Ile Pro Asn Arg Phe Phe Val Arg Ser Ser
                  1140                1145                1150
 25
      atg ttt gaa agt gag tgg gga ggg aac cta act att aac aaa gtc ata    3504
      Met Phe Glu Ser Glu Trp Gly Gly Asn Leu Thr Ile Asn Lys Val Ile
              1155                1160                1165

 30   aca agt cct gtt att aca gga gca cta act tct ata aga gga aat ttt    3552
      Thr Ser Pro Val Ile Thr Gly Ala Leu Thr Ser Ile Arg Gly Asn Phe
         1170                1175                1180

      aat tta cta gga aaa caa ttt tct ctt gct aaa agt aca ata tca ttt    3600
 35   Asn Leu Leu Gly Lys Gln Phe Ser Leu Ala Lys Ser Thr Ile Ser Phe
      1185                1190                1195                1200

      tca gga tca gtt cca cca aac cca cta ctc aat att tct tta aca tat    3648
      Ser Gly Ser Val Pro Pro Asn Pro Leu Leu Asn Ile Ser Leu Thr Tyr
 40               1205                1210                1215

      tca tca cct tct att aca gct ata ggc att att aaa ggt aca act agt    3696
      Ser Ser Pro Ser Ile Thr Ala Ile Gly Ile Ile Lys Gly Thr Thr Ser
                  1220                1225                1230
 45
      aat cct aat att act ttt tca agt aca cca cct tta cct caa gat gaa    3744
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                Asn Pro Asn Ile Thr Phe Ser Ser Thr Pro Pro Leu Pro Gln Asp Glu
                       1235                1240                1245


                ata gtt tcc caa gtt ctt ttt ggt aaa agc tca caa agt ctt agc agg    3792
        5       Ile Val Ser Gln Val Leu Phe Gly Lys Ser Ser Gln Ser Leu Ser Arg
                       1250                1255                1260


                ata caa gcc ata caa ctt gct caa gaa tta gca aac tta aca gga ttt    3840
                Ile Gln Ala Ile Gln Leu Ala Gln Glu Leu Ala Asn Leu Thr Gly Phe
        10      1265                1270                1275                1280


                aat act gga agt atg aat ttc cta aca aat att cga cag aca tta ggg    3888
                Asn Thr Gly Ser Met Asn Phe Leu Thr Asn Ile Arg Gln Thr Leu Gly
                           1285                1290                1295

        15
                tta gat ata ctt agc tta ggg aca act tct aat aga aaa gcc aat aca    3936
                Leu Asp Ile Leu Ser Leu Gly Thr Thr Ser Asn Arg Lys Ala Asn Thr
                       1300                1305                1310


        20      tcc aac tca aac gat caa ata gaa gat atc cct gtt ata gaa cta ggt    3984
                Ser Asn Ser Asn Asp Gln Ile Glu Asp Ile Pro Val Ile Glu Leu Gly
                       1315                1320                1325


                aaa tat att aca gac act gtt tat gtt ggt gtt gaa caa agt tat tta    4032
        25      Lys Tyr Ile Thr Asp Thr Val Tyr Val Gly Val Glu Gln Ser Tyr Leu
                       1330                1335                1340


                gat agt aat gat act ggg gca aga ata tca gtt gaa ctt gca cct aat    4080
                Asp Ser Asn Asp Thr Gly Ala Arg Ile Ser Val Glu Leu Ala Pro Asn
        30      1345                1350                1355                1360


                ttt aat ctt gaa ggt aga aca ggg act caa tat agt gag ata ggt att    4128
                Phe Asn Leu Glu Gly Arg Thr Gly Thr Gln Tyr Ser Glu Ile Gly Ile
                           1365                1370                1375

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                    20              25                  30

       Arg Thr Ser Thr Gly Ile Ala Trp Ile Lys Asn Thr Val Ser Ser Leu
                35              40                  45

 10    Leu Gln Gln Gln Gly Ile Ile Leu Gln Val Ser Ser Ile Ile Gly Pro
                50              55                  60

       Phe Pro Glu Gln Ile Thr Ile Asn Glu Leu Ser Leu Ser Asp Val Asn
            65              70              75                  80
 15
       Gly Thr Tyr Leu Thr Ile Ser Asn Leu Glu Ile Gln Ser Asn Leu Trp
                    85              90                  95

       Ala Leu Phe Lys Gly Gln Leu Glu Ile Leu Ser Phe Glu Leu Asn Asp
 20             100             105                 110

       Leu Val Leu Tyr Arg Leu Pro Ser Asn Asn Asn Leu Lys Lys Ser Ser
                115             120                 125

 25    Thr Ser Phe Val Leu Pro His Ile Ser Phe Asp Leu Thr Pro Trp Trp
                130             135                 140

       Thr Glu His Ile Arg Ile Gln Asn Ile His Ile Asn Asn Thr Gln Leu
            145             150             155                 160
 30
       Ser Ser Asp Ile Ile Gly Ile Pro Leu Val Leu Ser Leu Glu Gly Asp
                    165             170                 175

       Gly Thr Leu Thr Asn Trp Asn Gly Thr Phe Gln Leu Ser Ser Ser Asn
 35             180             185                 190

       Lys Thr Lys Ile Ile Gly Thr Leu Arg Tyr Gln Gly Asn Lys Thr Gln
                195             200             205

 40    Phe Phe Glu Tyr Val His Pro Thr Arg Ile Val Thr Leu Glu Ile Asp
                210             215             220

       Ser Val Ala Asp Lys Lys Ser Tyr Asn Asn Ser Ile Leu Glu Gln Pro
            225             230             235                 240
 45
       Leu His Leu His Leu Ser Ile Tyr Pro Glu His Asn Arg Ile Ile Leu
```

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245   250   255

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His Ser Leu Leu Ala Glu Tyr Gly Ser Trp Leu Leu Thr Ser Glu Ser
    260   265   270

5

Ile Glu Val Ser Asn Glu Gln Leu Lys Gly Asn Ile Leu Leu Lys Tyr
    275   280   285

Asn Gly Glu Ala Thr His Gln Leu Pro Ile Lys Lys Leu Asn Ser Ser
10   290   295   300

Ile Thr Leu Ser Gly Ser Leu Asn Lys Pro Asn Phe Ser Ile Gln Met
305   310   315   320

15 Thr Leu Pro Glu Ile Asn Ile Thr Lys Asn Ile Ile Asp Leu Gln Thr
      325   330   335

Glu Leu Val Ile Asn Leu Gly Leu Phe Ser Thr His Ser Asp Ile Leu
    340   345   350

20 Thr Ser Gly Thr Ile Thr Val Gln Gly Glu Thr Ile Pro Asn Ser Ile
    355   360   365

Leu Ser Ser Ala Val Asp Ile Ile Ala Ser Thr Thr Thr His Thr Ile
25   370   375   380

Thr Leu Glu His Ala Thr Leu Thr Ser Pro Glu Met His Phe Ser Leu
385   390   395   400

30 Ser Gly Glu Phe Asn Ser Leu Leu Gly Asn Ile Asp Ala Asn Leu Lys
      405   410   415

Gly Asn Thr Pro Thr Leu Ser Ile Phe Ser Ser Leu Leu Gly Leu Pro
    420   425   430

35

Asp Leu Thr Gly Gln Ser Asn Ile Thr Ile Gly Leu His Arg Gln Gly
    435   440   445

Ser Ser Ser Ser Ile Glu Gly Thr Ala Thr Val Ser Leu Asn Asn Met
40   450   455   460

Asn Trp Gly Val Gln Ala Leu Gln Gly Thr Leu Gly Asp Asn Ala Thr
465   470   475   480

45 Leu Ser Gly Ile Tyr Asn Leu Thr Pro Ile Asp Trp Ser Ile Ser Leu
      485   490   495

```
    Asn Lys Leu Lys Leu Thr Ala Lys Asn Val Tyr Ala Glu Gly Leu Ile
                500                 505             510

5   Asn Phe Gln Lys Lys Tyr Ile Asp Ser Ser Ile Asn Leu Ile Ile Pro
                515                 520             525

    Asn Leu Gln Leu Ile Ala Pro Pro Ile Ser Gly Glu Leu Gln Ser Leu
            530             535             540
10
    Ile Thr Val Ser Gly Lys Leu Asp Ala Pro Ser Ile Glu Ser Lys Ile
    545             550             555                 560

    Phe Ser Ser Gln Leu Thr Trp Asn Ala Leu Gln Leu Asn Asn Pro Gln
15              565             570             575

    Leu Ile Ile Thr Thr Thr Gln Ser Ser Ser Ser Ala Ile Lys Gly Asn
                580             585             590

20  Ile Thr Leu Ser Ala Glu Pro Ala Ser Ser Glu Ala Leu Thr Phe Ser
                595             600             605

    Ser Asn Trp Gly Ile Leu Pro Thr Glu Ile Leu Val Glu Lys Ile Ile
        610             615             620
25
    Gly Asn Ile Leu Gly Val Asn Leu Asp Gly Asn Ile Lys Ile Thr Lys
    625             630             635                 640

    Lys Asp Tyr Leu Ile Asn Gly Asp Ile Ile Ala Glu Val Gln Ser Trp
30              645             650             655

    Lys Asp Ile Ala Asn Ile Leu Gln Ile Pro Ile Arg Gly Ser Ala Ser
                660             665             670

35  Ile Lys Ile Gln Phe Asp Pro Lys Asn Gln Gln Cys Ile Ser Thr Gln
                675             680             685

    Trp Gln Leu Lys Asn Phe Ile Leu Gly Asn Asn Phe Asn Val Thr Thr
            690             695             700
40
    Ile Lys Gly Arg Ala Asp Thr Ile Gln Leu His Lys Asn Pro Thr Ile
    705             710             715                 720

    Ala Leu Ser Ser Lys Ile Gly Ala Gly Thr Tyr Glu Asp Phe Gln Trp
45              725             730             735
```

```
      Thr Gln Gly Thr Leu Asp Ile Lys Gly Thr Leu Lys Asn Phe Asn Ser
                  740             745                 750

  5   Lys Ile Asn Ile Ala Gly Gln Thr Thr Val Asn Ala Asn Phe Gln Thr
                  755             760                 765

      Asn Leu Phe Glu Lys Asn Ile Asn Ile Thr Thr Leu Asn Leu Lys Asn
                  770             775                 780

 10   Ile Gln Lys Asn Ile Gly Ile Lys Leu Leu Gln Pro Ile Lys Ile Ile
      785             790                 795                 800

      Val Ser Pro Gln Gln Phe Val Leu Asn Asn Cys Ser Leu Ala Ile Leu
                  805             810                 815

 15
      Pro Ser Gly Thr Ile Thr Thr Asp Ile Tyr Val Thr Pro Gln Arg Leu
                  820             825                 830

      Asn Ala Asn Ala Ile Ile Lys Glu Val Ser Leu Leu Ser Phe Gln Pro
 20               835             840                 845

      Phe Ser Ile Leu Leu Pro Gln Gly Asn Ile Asn Gly His Ile Thr Leu
          850             855                 860

 25   Thr Gly Ile Pro Ser Lys Pro Lys Gly Thr Leu Ser Phe Asp Ile Leu
      865             870                 875                 880

      Asn Ile His Tyr Pro Arg Pro Asn Pro Ser Ile Ala Asn Leu His Val
                  885             890                 895

 30
      Glu Gly Glu Ile Ile Ser Ser Pro Asn Asn Ile Cys Lys Leu Asn Ala
                  900             905                 910

      Thr Leu Thr Glu Lys Lys Glu Pro Ile Pro Ile Ser Ile Gln Ala Thr
 35               915             920                 925

      Leu Pro Phe Glu Phe Thr Glu Asn Asn Ile Pro Met Leu Ser Lys Met
          930             935                 940

 40   Arg Pro Phe Ser Ala His Ile Lys Trp Thr Gly Ile Leu Asp Thr Leu
      945             950                 955                 960

      Trp Lys Leu Ile Pro Leu Thr Asp Tyr Ile Met Ala Gly Asn Gly Ser
                  965             970                 975

 45
      Leu Asp Ala Ser Leu Ser Gly Thr Leu Asp Ser Pro Thr Tyr Ala Ile
```

```
                       980                 985                 990

      Ile Thr Thr Leu Ser Asn Ala Asn Phe Gln Asp Leu Ser Leu Gly Leu
                  995                 1000                1005
 5

      Tyr Leu Glu Asn Ile Asn Ala Lys Leu Gln Val Phe Ser Asn Arg Ile
             1010                1015                1020


      Ser His Ile Gln Ala Thr Ala Ser Asp Gly Lys Gln Gly Ser Ile Gln
10    1025                1030                1035                1040


      Leu Ile Gly Asn Ile Gly Ser Ser Lys Glu His Phe Pro Leu Ser Ile
                  1045                1050                1055


15    Asn Gly Ser Phe Thr Asn Leu Ala Pro Leu Gln Arg Lys Asp Leu Ser
                  1060                1065                1070


      Leu Thr Leu Ser Gly Ala Ala Thr Leu Glu Gly Thr Leu Lys Gln Ser
                  1075                1080                1085
20

      Glu Val Lys Gly Asp Ile Val Ile Asn Gln Gly Glu Phe Gln Leu Thr
             1090                1095                1100


      Glu Gly Leu Thr Ser Asn Ile Pro Thr Leu Asn Val Val Asp Ser Thr
25    1105                1110                1115                1120


      Gln Gln Gln Asn Thr Lys Thr Lys Lys Ala Thr Tyr Gln Gln Pro Thr
                  1125                1130                1135


30    Leu Ser Ile Ala Leu Ser Ile Pro Asn Arg Phe Phe Val Arg Ser Ser
                  1140                1145                1150


      Met Phe Glu Ser Glu Trp Gly Gly Asn Leu Thr Ile Asn Lys Val Ile
             1155                1160                1165
35

      Thr Ser Pro Val Ile Thr Gly Ala Leu Thr Ser Ile Arg Gly Asn Phe
             1170                1175                1180


      Asn Leu Leu Gly Lys Gln Phe Ser Leu Ala Lys Ser Thr Ile Ser Phe
40    1185                1190                1195                1200


      Ser Gly Ser Val Pro Pro Asn Pro Leu Leu Asn Ile Ser Leu Thr Tyr
                  1205                1210                1215


45    Ser Ser Pro Ser Ile Thr Ala Ile Gly Ile Ile Lys Gly Thr Thr Ser
                  1220                1225                1230
```

Asn Pro Asn Ile Thr Phe Ser Ser Thr Pro Pro Leu Pro Gln Asp Glu
    1235   1240   1245

5   Ile Val Ser Gln Val Leu Phe Gly Lys Ser Ser Gln Ser Leu Ser Arg
        1250   1255   1260

    Ile Gln Ala Ile Gln Leu Ala Gln Glu Leu Ala Asn Leu Thr Gly Phe
    1265   1270   1275   1280

10 Asn Thr Gly Ser Met Asn Phe Leu Thr Asn Ile Arg Gln Thr Leu Gly
                1285   1290   1295

    Leu Asp Ile Leu Ser Leu Gly Thr Thr Ser Asn Arg Lys Ala Asn Thr
15   1300   1305   1310

    Ser Asn Ser Asn Asp Gln Ile Glu Asp Ile Pro Val Ile Glu Léu Gly
            1315   1320   1325

20 Lys Tyr Ile Thr Asp Thr Val Tyr Val Gly Val Glu Gln Ser Tyr Leu
        1330   1335   1340

    Asp Ser Asn Asp Thr Gly Ala Arg Ile Ser Val Glu Leu Ala Pro Asn
    1345   1350 .   1355   1360

25 Phe Asn Leu Glu Gly Arg Thr Gly Thr Gln Tyr Ser Glu Ile Gly Ile
                1365   1370   1375

    Asn Trp Lys Lys Asp Tyr
30   1380

    <210> 19
    <211> 26
    <212> DNA
35 <213> Artificial Sequence

    <220>
    <223> Description of Artificial Sequence:
        Oligonucleotide probe/primer
40
    <400> 19
    catattcaag gtacagcatc tgatgg   26

    <210> 20
45 <211> 21
    <212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
5   Oligonucleotide probe/primer

<400> 20
ctcctttaca aaccttgctc c   21

10

<210> 21
<211> 22
<212> DNA
<213> Artificial Sequence

15

<220>
<223> Description of Artificial Sequence:
        Oligonucleotide probe/primer

20   <400> 21
gctcatctaa agaacacttt cc   22

<210> 22
25   <211> 23
<212> DNA
<213> Artificial Sequence

<220>
30   <223> Description of Artificial Sequence:
        Oligonucleotide probe/primer

<400> 22
caaggtagta tacaacttat tgg   23

35

<210> 23
<211> 23
<212> DNA
40   <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
        Oligonucleotide probe/primer

45

<400> 23

gacctaagtc ttacactttc agg   23


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    <210> 24
5   <211> 24
    <212> DNA
    <213> Artificial Sequence


    <220>
10  <223> Description of Artificial Sequence:
         Oligonucleotide probe/primer


    <400> 24
    gtattaatac tacattagtt gacg                                 24
15


    <210> 25
    <211> 21
    <212> DNA
20  <213> Artificial Sequence


    <220>
    <223> Description of Artificial Sequence:
         Oligonucleotide probe/primer
25
    <400> 25
    ggataataat ggaaaaagtg g                                    21


30  <210> 26
    <211> 22
    <212> DNA
    <213> Artificial Sequence


35  <220>
    <223> Description of Artificial Sequence:
         Oligonucleotide probe/primer


    <400> 26
40  caagcaatgc ctgtagaggt cc                                   22


    <210> 27
    <211> 24
45  <212> DNA
    <213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:
     Oligonucleotide probe/primer

5

<400> 27
aagaatgcct gtaataataa gtcc   24

10 <210> 28
    <211> 19
    <212> DNA
    <213> Artificial Sequence

15 <220>
    <223> Description of Artificial Sequence:
         Oligonucleotide probe/primer

    <400> 28
20 ttggggaatc ctacctacg   19

    <210> 29
    <211> 21
25 <212> DNA
    <213> Artificial Sequence

    <220>
    <223> Description of Artificial Sequence:
30   Oligonucleotide probe/primer

    <400> 29
    tattaggagt aaatcttgat g   21

35

    <210> 30
    <211> 22
    <212> DNA
    <213> Artificial Sequence
40
    <220>
    <223> Description of Artificial Sequence:
         Oligonucleotide probe/primer

45 <400> 30
    gcaggacaaa caactgtaaa cg   22

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<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide probe/primer

<400> 31
gaggaagaag tatactaaat gg                                           22


<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide probe/primer

<400> 32
tgttggacta tctaaagtcc                                              20


<210> 33
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide probe/primer

<400> 33
ctattgatgg atttggcctt gg                                           22


<210> 34
<211> 20                                                  <212>
DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence:
      Oligonucleotide probe/primer

5   <400> 34
     gtgctggtac atatgaagac   20

     <210> 35
10   <211> 20
     <212> DNA
     <213> Artificial Sequence

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15   <223> Description of Artificial Sequence:
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     <400> 35
     ttcatcacct tctattacag   20
20

     <210> 36
     <211> 20
     <212> DNA
25   <213> Artificial Sequence

     <220>
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           Oligonucleotide probe/primer
30
     <400> 36
     ggaaactatt tcatcttgag   20

35   <210> 37
     <211> 20
     <212> DNA
     <213> Artificial Sequence

40   <220>
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           Oligonucleotide probe/primer

     <400> 37
45   attaggtgca agttcaactg   20

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<210> 38
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
     Oligonucleotide probe/primer

<400> 38
tttagatagt aatgatactg                                           20


<210> 39
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
     Oligonucleotide probe/primer

<400> 39
ttattatatt atgttttttg taatgttaat ttcagg                          36


<210> 40
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
     Oligonucleotide probe/primer

<400> 40
gacatatgaa taacacaaaa atactttc                                   28


<210> 41
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
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   <223> Description of Artificial Sequence:
         Oligonucleotide probe/primer


   <400> 41
 5 gaggatcctc tagagttaat caaactgtat ttttattgat g                    41



   <210> 42
   <211> 31
10 <212> DNA
   <213> Artificial Sequence


   <220>
   <223> Description of Artificial Sequence:
15         Oligonucleotide probe/primer


   <400> 42
   gacatatgcg gacctctaca ggcattgctt g                               31


.20

   <210> 43
   <211> 24
   <212> DNA
   <213> Artificial Sequence
25

   <220>
   <223> Description of Artificial Sequence:
         Oligonucleotide probe/primer

30 <400> 43
   gatcaggtag tccaagaaga gaag                                       24



   <210> 44
35 <211> 45
   <212> DNA
   <213> Artificial Sequence


   <220>
40 <223> Description of Artificial Sequence:
         Oligonucleotide probe/primer


   <400> 44
   ttggaggatc ctctagagtt atcaggttgt aattgttcca gatgg                45
45
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<210> 45
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
        Oligonucleotide probe/primer

<400> 45
ccttggttaa taacaatatc g   21

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
        Oligonucleotide probe/primer

<400> 46
caactccact tcaagataga agc   23

<210> 47
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligo

<400> 47
gaccatggaa aaagtatgtt attttttttc   29

<210> 48
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligo

<400> 48
gaggatcctc tagagttaga atgcttgccc aatact   36

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<210> 49
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligo

<400> 49
ttggaggatc ctctagagtt agaatgcttg cccaatact                          39


<210> 50
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligo

<400> 50
ttgaccatgg ctacatcaat taccacttcc ac                                32


<210> 51
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligo

<400> 51
ggacatatga ataacacaaa aatactttc                                    29


<210> 52
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: oligo

<400> 52
ttggaggatc ctctagagtt aatcaaactg tatttttatt gatg                   44


<210> 53
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<211> 32
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: oligo


<400> 53
ggacatatgc ggacctctac aggcattgct tg                          32


<210> 54
<211> 20
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: oligo


<400> 54

tgaggattat taagttggag                                        20


<210> 55
<211> 20
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: oligo


<400> 55
gcatgcaacc ttaacatctc                                        20


<210> 56
<211> 20
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: oligo


<400> 56
tttctgatgt aagtaaccag                                        20


<210> 57
<211> 20
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```
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: oligo


<400> 57
tctgcccata tcaagtggac                                              20


<210> 58
<211> 20
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: oligo


<400> 58
ggaacatttc aactatcctc                                             20


<210> 59
<211> 28
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: oligo
<400> 59
gtaaggtaag ttccattcac                                             20


<210> 60
<211> 25
<212> DNA
<213> Artificial Sequence


<220>
<223> Description of Artificial Sequence: oligo


<400> 60
caacgtggat ccgaattcaa gcttc                                       25



<210> 61
<211> 17
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Peptide

<400> 61
Met Gly Ser Gly Ser Gly Asp Asp Asp Asp Lys Leu Ala Leu Leu Thr
 1   5   10   15

Met

<210> 62
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 62
Ala Thr Ser Ile Thr Thr Ser
 1   5

<210> 63
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 63
Met His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
 1   5   10   15

Gly Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp
            20   25   30

Ser Pro Asp Leu Gly Thr Asp Asp Asp Asp Lys Ala Met
            35   40   45

<210> 64
<211> 50

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 64
Met His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
  1   5   10   15

Gly Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp
                20   25   30

Ser Pro Asp Leu Gly Thr Asp Asp Asp Asp Lys Ala Met Ala Asp Ile
                35   40   45

Gly Ser
      50

<210> 65
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 65
Glu Phe Asn Leu Ser Lys Gly
  1   5

<210> 66
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 66
Met Gly Ser Gly Ser Gly Asp Asp Asp Asp Lys Leu Ala Leu Gly His
  1   5   10   15

Met

<210> 67
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 67
Arg Thr Ser Thr Gly Ile Ala
 1   5

<210> 68
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 68
Asp Pro Asn Ser Ser Ser Val Asp Lys Leu Ala Ala Ala Leu Glu His
 1   5   10   15

His His His His His
            20